

GenCore version 4.5
Copyright (c) 1993 - 2000 Computer Ltd.

OM nucleic - nucleic search using sw model

Run on: July 25, 2002, 15:12.03, Search time 1772.54 seconds

(without alignments)
12444.058 Million cell updates/sec

Title: US-09-601-371-1

Perfect score: 1621

Sequence: 1 agagatattatataaadaa.....tataaadaaadaaadaaadaa 1621

Scoring table: IDENTITY_NUC
GapP 10.0, GapExt 1.0

Searched: 15746207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 2742411

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

EST:*

1: em_estba:*

2: em_estbm:*

3: em_estin:*

4: em_estnu:*

5: em_estor:*

6: em_estpl:*

7: em_estro:*

8: em_hre:*

9: qb_est1:*

10: qb_est2:*

11: qb_hre:*

12: qb_gss:*

13: em_gss_hum:*

14: em_gss_inv:*

15: em_gss_pln:*

16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY:

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 119.4 | 7.4 | 1101 | 12 | CNS00211 |
| 2 | 114.9 | 7.1 | 1095 | 10 | BE120715 |
| 3 | 113.2 | 7.0 | 1145 | 12 | CNS00350 |
| 4 | 110.2 | 6.8 | 924 | 10 | BH415947 |
| 5 | 110.2 | 6.8 | 1036 | 12 | CNS03181 |
| 6 | 109.4 | 6.7 | 848 | 3 | B1644518 |
| 7 | 109.4 | 6.7 | 944 | 10 | BH416130 |
| 8 | 109.4 | 6.7 | 1042 | 12 | CNS0148K |
| 9 | 109.2 | 6.7 | 910 | 10 | BH415636 |
| 10 | 109 | 6.7 | 922 | 12 | A548363 |
| 11 | 108.6 | 6.7 | 966 | 10 | BH415486 |
| 12 | 108.4 | 6.7 | 798 | 3 | B1645911 |
| 13 | 108.2 | 6.7 | 924 | 12 | B123297 |
| 14 | 108.2 | 6.7 | 1101 | 12 | CNS009112 |
| 15 | 108 | 6.7 | 840 | 3 | B1645072 |
| 16 | 106.2 | 6.4 | 748 | 12 | A5031854 |
| 17 | 106.2 | 6.6 | 1149 | 12 | A2997537 |

| | | | | | |
|----|-------|-----|------|----|----------|
| 18 | 105.8 | 6.3 | 1141 | 12 | CNS00441 |
| 19 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 20 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 21 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 22 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 23 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 24 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 25 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 26 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 27 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 28 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 29 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 30 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 31 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 32 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 33 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 34 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 35 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 36 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 37 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 38 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 39 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 40 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 41 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 42 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 43 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 44 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |
| 45 | 104.8 | 6.2 | 1141 | 12 | CNS00441 |

ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SEQUENCE

QUALITY

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JOURNAL
COMMENT

Unpublished (2001)
Contact: Opperman, R
Center for the Biology of Nematode Parasitism
NC State University, IACR-Rothamsted
Campus Box 7616, Raleigh, NC 27695, USA
Tel: 919.515.6699
Tel: 919.515.6590
Fax: 919.515.6590
Email: warrhof@unity.ncsu.edu
GILIPS# F06 1-408 047-061.

FEATURES

Local non/Qualifiers
1. 1964
/organism "Gloabaster pallida"
/db_xref "taxon:6090"
/zoo_lib "Mixed Stage ESTs from Gloabaster pallida, the potato cyst nematode"
/to "Gloabaster pallida" and this is a database off set
between JACR-Rothmund and North Carolina State
University. The library was constructed from mixed stage
G. pallida in lambda cIII by Paul Burroughs,
JACR-Rothmund."

| BASE COUNT | 42 d | 46 d | 48 d | 85 d | 16 others |
|-------------------|------|------|------|------|-----------|
| BACK ROT TRANSFER | | | | | |

Query Match 6.78; Score 109.4; DB 10; Length 964;
Best Local Similarity 46.68; Pred. No. 3.3e-05;
Matches 400; Coverage 100%; Missed Reads 0

[illegible]

1b 262 AAAAAAAAAAAAAAAAAAAGGAGGCTTCCAAAAAAAAAAAAAAAA 217

RESULT

| | |
|------------|--|
| RESULT | 8 |
| LOCUS | CNS0148K/c |
| DEFINITION | CNS0148K 1042 bp BWA library: GSS-26-JUL-1999 <i>Drosophila melanogaster</i> genome survey sequence S96 end of BAC BAC116 of proBAC library from <i>Drosophila melanogaster</i> (fruit fly) genomic survey sequence |

ACCESSION

| | |
|-----------|------------|
| ACCESSION | AL103838 |
| VERSION | AL103838.1 |
| KEYWORDS | GSS. |

THE

SOURCE
ORGANISM
fruit fly.
Drosophila melanogaster
Ergas et al., 1970; Ergas et al., 1968; Ergas;
Prybylka, Neoptera; Endopterygota; Diptera; Brachycera;
Mesomorpha; Ephyraidea; Protophyllidae; Drosophylla.
1 (bases 1 to 1042)

AUTHORS

AUTHORS
Genoscope, Centre National de Séquençage ;
Direct Submission
Submitted (23 JUL 1999) Genoscope
JP 191 91006 EVRY cedex - FRANCE (E-mail : secretairegenoscope.cns.fr
- web : www.genoscope.cns.fr)

COMMENT

COMMENT: determination of this BAC end sequence was carried out as part of a collaboration with the European Biosophila Genome Project (EBGP) (<http://www.ebpg.org>) and this *inrosophila melanogaster* BAC library (Dros BAC) was made by Alain Hillard at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a research project grant. The DNA was prepared from embryos by Alain Hucheton and Christophe Payan. It has been constructed in the vector pBluescriptII.

FLYING

```

FLATHEADS
  # of flathead flatters
  1, 1042
  /organism "Proscopila melanogaster"
  /plasmid "pBeloHAC1"
  db_xref :taxon, 7227
  clone_lib "prosbac"
  /clone "BACN116"
  version 1.0

```

| BASE: COUNCIL | 68 a | 55 c | 41 q | 690 t | 188 others |
|---------------|------|------|------|-------|------------|
| ORIGIN | | | | | |

Query Match 6.7%, Score 199.4, PE 12, Length 1042
Best Local Similarity 40.7%; Pred. No. 3.2e-05;
Matches 33; Conservative 50; Mismatches 427; Indels 0;

[illegible]

DB 904 SAAACAAAGCSVHTMARAAAAMMATMKAAMAKMACATMAWTASMAWMTSAAAGTGAMIAATV 845

[illegible]

100 R44 TAAVSCMNCMMWYAAATSAMGAGAAASSMGGAAAWNTYHCCAATTHARGMAAAWGAAGA 789

Q 798 .t13aaat1caaacccacafqtatatctttatctttttatcttttttqaccctgtactacatttgaagcttta 857

14) 784 (A)AAH1WA3T1MWAKATASAAA1WAMSAK0AAAAAAMAS1SRTCSMAWMAAAWTAQSW / 21

07 858 aut laqcaacaaupl caataqtat qqlt qact caqccadqqat qat la 917

DB 724 AAAATGCTAAATTACAGGCHAAAGSATTGMAWAMCAGRAATATCATCTGACSCATGACATAC 669

[illegible]

604 TGAATGTTTMAAAAGAGTGGGAAATTATATGATTTTATTAAGGACATTTGAAAAA 605
 606

[illegible][illegible]

604 AAAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

[illegible]


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CY 1194 aaatattatattgaaaggtttaaagagtgtaattgaattatattatga 1254
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 526 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 467
CY 1264 aaatttgaagaaatatttgcgtatttgaagaaatgcgaaatatttga 1314
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 406 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 407
CY 1314 ctgaagaatattcctgaattttttttttttaaataaagaagaatattt 1374
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 406 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 407
CY 1374 tttaagaagaattadagaacagtttttcgttttttttttttttttt 1434
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 546 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 287
CY 1444 aaagaattttgaagaaatgcgtaaagaagaagaatttgaagaataga 1494
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 286 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 227
CY 1494 aaattatttgaatttttgaattttgaattttgaattttgaattttga 1554
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 226 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 167
CY 1554 atatttcagtttttgaatttgaattttgaattttgaattttgaatt 1614
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 166 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 107
CY 1614 aaagaaga 1621
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 106 AAAAAAAAAA 99

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PF001 13

BI645011/c standard: KNA: EST: 788 BP.

XX BI645011

AC BI645011

SV BI645011.1

XX 13-SEP-2001 (Rel. 69, Created)

DI 13-SEP-2001 (Rel. 69, Last updated, Version 1)

XX 092810 Mixed Stage EST's from Globodera pallida, the potato cyst nematode

DE Globodera pallida CERA, mHNA seq. data.

XX EST.

XX Globodera pallida

XX Eukaryota: Metazoa: Nemata: Tylenchida, Tylenchida, Tylenchida;

XX Tylenchoidea: Heteroderidae: Heteroderinae: Globodera.

XX [1]

XX 1-788

RA Heer J., Sosinski B., Pokrzywa P.M., Wary A., Opperman G.

PI "Mixed Stage EST's from Globodera pallida, the potato cyst nematode";

RL Unpublished.

XX Contact: Opperman, G

XX Center for the Biology of Nematode Parasitism

XX NC State University, 4670 Rothamsted

XX Campus Box 7616, Raleigh, NC 27695, USA

XX Tel: 919.515.5699

XX Fax: 919.515.9500

XX Email: warthen@biology.ncsu.edu

XX No homology found. : GI11-6PCN_F_107_PCN_F_058.dbl.seq.screen.

XX Key Location/Qualifiers

XX 1-788

XX /db_xref="taxon:36090"

XX /note="Vector: lambda GT11; This is a collaborative effort

XX

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CY 1194 aaatattatattgaaaggtttaaagagtgtaattgaattatattatga 1254
 DB 526 AA 467
 CY 1264 aaatttgaagaaatatttgcgtatttgaagaaatgcgaaatatttga 1314
 DB 406 AA 407
 CY 1314 ctgaagaatattcctgaattttttttttttaaataaagaagaatattt 1374
 DB 406 AA 407
 CY 1374 tttaagaagaattadagaacagtttttcgttttttttttttttttt 1434
 DB 546 AA 287
 CY 1444 aaagaattttgaagaaatgcgtaaagaagaagaatttgaagaataga 1494
 DB 286 AA 227
 CY 1494 aaattatttgaatttttgaattttgaattttgaattttgaattttga 1554
 DB 226 AA 167
 CY 1554 atatttcagtttttgaatttgaattttgaattttgaattttgaatt 1614
 DB 166 AA 107
 CY 1614 aaagaaga 1621
 DB 106 AAAAAAAAAA 99

Query Map:

Best local similarity: 45.0% (Seq. ID: 100.0%)

Matches: 256 (5.0%) (Seq. ID: 100.0%)

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Genome version 4.5
Copyright (c) 1998 - 2000 Compugen Ltd.

1M protein protein search, using sw model

Run on: July 24, 2002, 14:31:32 / Search time 31.17 seconds
(without alignments)
2755.420 Million cell updates/sec

Title: US-09-601-371-2
Perfect score: 2189
Sequence: 1 M995971121SLSP1A1106

Scoring table: BLAST62
Gapop 10.0 / Gapext 0.5

Search: 1 62222 seqs, 17294529 residues
total number of hits satisfying chosen parameters: 952222

Minimum DB seq length: 0
Maximum DB seq length: 2409000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1 SVTMBL139

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_murci:*
- 8: sp_orseae:*
- 9: sp_plant:*
- 10: sp_protist:*
- 11: sp_virus:*
- 12: sp_vertebrate:*
- 13: sp_unclassified:*
- 14: sp_virus:*
- 15: sp_bacteriophage:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-----------|----------------------|
| 1 | 2189 | 100.0 | 428 | 2 032417 | 032417 mycoplasma |
| 2 | 2181 | 99.8 | 429 | 2 098386 | 098386 mycoplasma |
| 3 | 2178.5 | 99.5 | 429 | 2 098384 | 098384 mycoplasma |
| 4 | 2175 | 99.4 | 429 | 2 098387 | 098387 mycoplasma |
| 5 | 2174.5 | 99.3 | 429 | 2 098386 | 098386 mycoplasma |
| 6 | 2171 | 99.3 | 428 | 2 098386 | 098386 mycoplasma |
| 7 | 2173 | 99.3 | 428 | 2 098383 | 098383 mycoplasma |
| 8 | 2154 | 98.4 | 428 | 2 052311 | 052311 mycoplasma |
| 9 | 552 | 25.2 | 185 | 2 P44972 | P44972 mycoplasma |
| 10 | 462 | 21.1 | 461 | 16 098015 | 098015 mycoplasma |
| 11 | 442 | 20.3 | 455 | 2 098755 | 098755 mycoplasma |
| 12 | 421 | 19.2 | 457 | 2 048932 | 048932 mycoplasma |
| 13 | 225.5 | 13.3 | 350 | 16 099284 | 099284 streptococcus |
| 14 | 225 | 13.3 | 350 | 16 097880 | 097880 streptococcus |
| 15 | 212 | 9.7 | 349 | 2 094311 | 094311 streptococcus |
| 16 | 215.5 | 9.4 | 346 | 16 092556 | 092556 rhizobium m |

ALIGNMENTS

RESULT 1

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|----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032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 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032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 032417 | 03241 |
|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|----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RL Patient number JP1997157295-A/1.
 RL 17-JUN-1997 KAKAO CLONING SHINKO JET-EAR
 DR EMBL: 164084; BAA23540.1; -
 DR EMBL: A026157; BAA77211.2; -
 DR InterPro: IPR003760; Bmp.
 DR Pfam: PF02608; Bmp; 1.
 SQ SEQIDPACT 429 AA; 479.2 MW; 1449999210A34E C8564.

Query Match 100.0%; Score 2189; DB 2; Length 428;
 Best local similarity 100.0%; Pred. No. 218; 138;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPEKRLGLSLSPAAALPAAVAVSGNNPSSPKKAKGKSYLLINANPKQVFNNAELL 60
 DB 1 MPEKRLGLSLSPAAALPAAVAVSGNNPSSPKKAKGKSYLLINANPKQVFNNAELL 60
 QY 61 KLEPVLTPQKIKPKSPQSAIEALKAKINQKQIGKINNVHSSNPFSSAYNSALSACHKI 120
 DB 61 KLEPVLTPQKIKPKSPQSAIEALKAKINQKQIGKINNVHSSNPFSSAYNSALSACHKI 120
 QY 121 WUNGPQKQSTIKQYDAHPPELEPNQIKIGIDPEIDETEPYFWYSLQFNTPESAPFTGY 180
 DB 121 WUNGPQKQSTIKQYDAHPPELEPNQIKIGIDPEIDETEPYFWYSLQFNTPESAPFTGY 180
 QY 181 ATASWLSQFESKRVASFGSAFEGVITFNENFAPGGLYNNKPKSSKDYPISSVVLDS 240
 DB 181 ATASWLSQFESKRVASFGSAFEGVITFNENFAPGGLYNNKPKSSKDYPISSVVLDS 240
 QY 241 GFTAGKMNIVNNVLSSTPDAVKYNPHVILSVAGPATFETVRLANKGYVIGVSDQGM 300
 DB 241 GFTAGKMNIVNNVLSSTPDAVKYNPHVILSVAGPATFETVRLANKGYVIGVSDQGM 300
 QY 301 LQKQWHLISVLRKPEAVVETITGLISVAVYVAVVWVKKPKKPSGSGGCKPKKMG 360
 DB 301 LQKQWHLISVLRKPEAVVETITGLISVAVYVAVVWVKKPKKPSGSGGCKPKKMG 360
 QY 361 VARENSNLEQAKINNKIFEAEMKELPEFVAYINSEALFKCNINVSFLEALI 420
 DB 361 VARENSNLEQAKINNKIFEAEMKELPEFVAYINSEALFKCNINVSFLEALI 420
 QY 421 SAINKAAK 428
 DB 421 SAINKAAK 428

RESULT 2
 QYRGX5 ID QYRGX5 PRELIMINARY; PPT: 429 AA.
 AC QYRGX5
 DT 01-MAY-2000 (FEBRELL, 13, Created)
 DT 01-MAY-2000 (FEBRELL, 13, Last sequence update)
 DT 01-JUN-2001 (FEBRELL, 17, Last annotation update)
 DE MACROPHAGE ACTIVATING LIPOPROTEIN 404 PRECURSOR.
 GN MALP.
 OS Mycoplasma fermentans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OX Mycoplasmataceae; Mycoplasma.
 CX NCBI TaxID=2115;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN SK5;
 EX MEDLINE 99115554; PubMed 9916088;
 FA Calvert M.J., Kim M.P., Karpas A.P., Mahlap P.P., Wise K.S.;
 RI Differential posttranslational processing confers intraspecies
 RI variation of a major surface lipoprotein and a macrophage-activating
 RI lipopeptide of Mycoplasma fermentans.";
 RL Infect. Immun. 67:760-771(1999).
 DR EMBL: AF094211; AAD16396.1; -
 DR InterPro: IPR003760; Bmp.
 DR Pfam: PF02608; Bmp; 1.
 DR Signal: Lipoprotein.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 429 MACROPHAGE ACTIVATING LIPOPROTEIN-404.
 SQ SEQUENCE 429 AA; 479.2 MW; 1449999210A34E C8564.

FT CHAIN 25 428 MACROPHAGE ACTIVATING LIPOPROTEIN-404.
 SQ SEQUENCE 429 AA; 479.2 MW; 1449999210A34E C8564.

Query Match 99.9%; Score 2184; DB 2; Length 428;
 Best local similarity 99.8%; Pred. No. 2178; 118;
 Matches 427; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPEKRLGLSLSPAAALPAAVAVSGNNPSSPKKAKGKSYLLINANPKQVFNNAELL 60
 DB 1 MPEKRLGLSLSPAAALPAAVAVSGNNPSSPKKAKGKSYLLINANPKQVFNNAELL 60
 QY 61 KLEPVLTPQKIKPKSPQSAIEALKAKINQKQIGKINNVHSSNPFSSAYNSALSACHKI 120
 DB 61 KLEPVLTPQKIKPKSPQSAIEALKAKINQKQIGKINNVHSSNPFSSAYNSALSACHKI 120
 QY 121 WUNGPQKQSTIKQYDAHPPELEPNQIKIGIDPEIDETEPYFWYSLQFNTPESAPFTGY 180
 DB 121 WUNGPQKQSTIKQYDAHPPELEPNQIKIGIDPEIDETEPYFWYSLQFNTPESAPFTGY 180
 QY 181 ATASWLSQFESKRVASFGSAFEGVITFNENFAPGGLYNNKPKSSKDYPISSVVLDS 240
 DB 181 ATASWLSQFESKRVASFGSAFEGVITFNENFAPGGLYNNKPKSSKDYPISSVVLDS 240
 QY 241 GFTAGKMNIVNNVLSSTPDAVKYNPHVILSVAGPATFETVRLANKGYVIGVSDQGM 300
 DB 241 GFTAGKMNIVNNVLSSTPDAVKYNPHVILSVAGPATFETVRLANKGYVIGVSDQGM 300
 QY 301 LQKQWHLISVLRKPEAVVETITGLISVAVYVAVVWVKKPKKPSGSGGCKPKKMG 360
 DB 301 LQKQWHLISVLRKPEAVVETITGLISVAVYVAVVWVKKPKKPSGSGGCKPKKMG 360
 QY 361 VARENSNLEQAKINNKIFEAEMKELPEFVAYINSEALFKCNINVSFLEALI 420
 DB 361 VARENSNLEQAKINNKIFEAEMKELPEFVAYINSEALFKCNINVSFLEALI 420
 QY 421 SAINKAAK 428
 DB 421 SAINKAAK 428

RESULT 3
 QYRGX4 ID QYRGX4 PRELIMINARY; PPT: 429 AA.
 AC QYRGX4
 DT 01-MAY-2000 (FEBRELL, 13, Created)
 DT 01-MAY-2000 (FEBRELL, 13, Last sequence update)
 DT 01-JUN-2001 (FEBRELL, 17, Last annotation update)
 DE MACROPHAGE ACTIVATING LIPOPROTEIN-404 PRECURSOR.
 GN MALP.
 OS Mycoplasma fermentans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OX Mycoplasmataceae; Mycoplasma.
 CX NCBI TaxID=2115;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN MT-2;
 EX MEDLINE 99115554; PubMed 9916088;
 FA Calvert M.J., Kim M.P., Karpas A.P., Mahlap P.P., Wise K.S.;
 RI Differential posttranslational processing confers intraspecies
 RI variation of a major surface lipoprotein and a macrophage-activating
 RI lipopeptide of Mycoplasma fermentans.";
 RL Infect. Immun. 67:760-771(1999).
 DR EMBL: AF094212; AAD16396.1; -
 DR InterPro: IPR003760; Bmp.
 DR Pfam: PF02608; Bmp; 1.
 DR Signal: Lipoprotein.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 429 MACROPHAGE ACTIVATING LIPOPROTEIN-404.
 SQ SEQUENCE 429 AA; 479.2 MW; 1449999210A34E C8564.

Query Match 99.5%; Score 2178.5; DB 2; Length 429;


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QY 121 WVINDEPRLSIFQYIDAGREELFRNQIKIQTGDIETETKWEYSLEFNKESAFITGY 180
  |||
DB 121 WVLNGFABUSKQYIDAGREELFRNQIKIQTGDIETETKWEYSLEFNKESAFITGY 180
  |||
QY 181 ATASWISQWESKPPVAVSPGQAFPCVTFNDEFAKGIYYNQKHFSSKIYHTSPVKIDS 240
  |||
DB 181 ATASWISQWESKPPVAVSPGQAFPCVTFNDEFAKGIYYNQKHFSSKIYHTSPVKIDS 240
  |||
QY 241 GPTAGKMNIVNNVLSSTPAWKNPHVILSVAGIATFETVRLANKQYVIGVNSQGM 300
  |||
DB 241 GPTAGKMNIVNNVLSSTPAWKNPHVILSVAGIATFETVRLANKQYVIGVNSQGM 300
  |||
QY 301 IQDQPIILSVLHIFPCAVYETILIMLETFEEDYCYVVFQFALPKWHSHEGLQFQWIG 360
  |||
DB 301 IQDQPIILSVLHIFPCAVYETILIMLETFEEDYCYVVFQFALPKWHSHEGLQFQWIG 360
  |||
QY 361 GVAREHNSFEQAKINNKTEKATKMKELPELQVAYINSQKALEQINKIDNVSERLFAII 420
  |||
DB 361 GVAREHNSFEQAKINNKTEKATKMKELPELQVAYINSQKALEQINKIDNVSERLFAII 420
  |||
QY 421 SAINKAAK 428
  |||
DB 421 SAINKAAK 428
  |||

RESULT 6
QYRNG PRELIMINARY: PRT: 428 AA.
AC QYRNG
DT 01-MAY-2000 (FEMREL: 13, Created)
DT 01-MAY-2000 (FEMREL: 13, Last sequence update)
DT 01-JUN-2001 (FEMREL: 18, Last annotation update)
DE LIPOPEPTIDE ACTIVATING LIPID-PROTEIN-403 PEPTIDESOR.
GN MALP.
OS Mycoplasma fermentans.
SC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
CX N61_TaxID:2115;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN K7;
RA MEDLINE 9411554; PubMed 9916088;
RX Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
RT "Differential posttranslational processing confers intraspecies
  variation of a major surface lipoproteins and a macrophage-activating
  lipopeptide of Mycoplasma fermentans.";
KL Infect. Immun. 67:760-771(1999).
DE EMRL; AF099213; AAD16397.1;
DR InterPro: IPR003760; Bmp;
DR Pfam: PF02608; Bmp; 1.
KW Signal; Lipoprotein.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 38 MACROPHAGE ACTIVATING LIPID-PROTEIN 403.
SQ SEQUENCE 428 AA: 47875 MW: 59482.47228475003664;

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Query Match 99.48; Score 2174; DB 2; Length 428;
Best local Similarity 99.48; Pred. No. 10-117;
Matches 425; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MKRSKKILLGLSPAAILLAVAVSGNNINSEISSEKFIKSYTTINANGKQVKNNAELL 60
  |||
DB 1 MKRSKKILLGLSPAAILLAVAVSGNNINSEISSEKFIKSYTTINANGKQVKNNAELL 60
  |||
QY 61 KLRVLIIDKSKIDKSNQSAFAEALKAIRKQIGIEIRNVHESNEISAYNSALSAGHKI 120
  |||
DB 61 KLRVLIIDKSKIDKSNQSAFAEALKAIRKQIGIEIRNVHESNEISAYNSALSAGHKI 120
  |||
QY 121 WVINDEPRLSIFQYIDAGREELFRNQIKIQTGDIETETKWEYSLEFNKESAFITGY 180
  |||
DB 121 WVLNGFABUSKQYIDAGREELFRNQIKIQTGDIETETKWEYSLEFNKESAFITGY 180
  |||
QY 181 ATASWISQWESKPPVAVSPGQAFPCVTFNDEFAKGIYYNQKHFSSKIYHTSPVKIDS 240
  |||
DB 181 ATASWISQWESKPPVAVSPGQAFPCVTFNDEFAKGIYYNQKHFSSKIYHTSPVKIDS 240
  |||

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DB 121 WVINDEPRLSIFQYIDAGREELFRNQIKIQTGDIETETKWEYSLEFNKESAFITGY 180
  |||
QY 181 ATASWISQWESKPPVAVSPGQAFPCVTFNDEFAKGIYYNQKHFSSKIYHTSPVKIDS 240
  |||
DB 181 ATASWISQWESKPPVAVSPGQAFPCVTFNDEFAKGIYYNQKHFSSKIYHTSPVKIDS 240
  |||
QY 241 GPTAGKMNIVNNVLSSTPAWKNPHVILSVAGIATFETVRLANKQYVIGVNSQGM 300
  |||
DB 241 GPTAGKMNIVNNVLSSTPAWKNPHVILSVAGIATFETVRLANKQYVIGVNSQGM 300
  |||
QY 301 IQDQPIILSVLHIFPCAVYETILIMLETFEEDYCYVVFQFALPKWHSHEGLQFQWIG 360
  |||
DB 301 IQDQPIILSVLHIFPCAVYETILIMLETFEEDYCYVVFQFALPKWHSHEGLQFQWIG 360
  |||
QY 361 GVAREHNSFEQAKINNKTEKATKMKELPELQVAYINSQKALEQINKIDNVSERLFAII 420
  |||
DB 361 GVAREHNSFEQAKINNKTEKATKMKELPELQVAYINSQKALEQINKIDNVSERLFAII 420
  |||
QY 421 SAINKAAK 428
  |||
DB 421 SAINKAAK 428
  |||

RESULT 7
QYRNG PRELIMINARY: PRT: 428 AA.
AC QYRNG
DT 01-MAY-2000 (FEMREL: 13, Created)
DT 01-MAY-2000 (FEMREL: 13, Last sequence update)
DT 01-JUN-2001 (FEMREL: 17, Last annotation update)
DE MACROPHAGE ACTIVATING LIPID-PROTEIN-403 PEPTIDESOR.
GN MALP.
OS Mycoplasma fermentans.
SC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
CX N61_TaxID:2115;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN K7;
RA MEDLINE 9411554; PubMed 9916088;
RX Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
RT "Differential posttranslational processing confers intraspecies
  variation of a major surface lipoproteins and a macrophage-activating
  lipopeptide of Mycoplasma fermentans.";
KL Infect. Immun. 67:760-771(1999).
DE EMRL; AF099213; AAD16397.1;
DR InterPro: IPR003760; Bmp;
DR Pfam: PF02608; Bmp; 1.
KW Signal; Lipoprotein.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 38 MACROPHAGE ACTIVATING LIPID-PROTEIN 403.
SQ SEQUENCE 428 AA: 47875 MW: 59482.47228475003664;

```

```

Query Match 99.48; Score 2174; DB 2; Length 428;
Best local Similarity 99.48; Pred. No. 10-117;
Matches 425; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MKRSKKILLGLSPAAILLAVAVSGNNINSEISSEKFIKSYTTINANGKQVKNNAELL 60
  |||
DB 1 MKRSKKILLGLSPAAILLAVAVSGNNINSEISSEKFIKSYTTINANGKQVKNNAELL 60
  |||
QY 61 KLRVLIIDKSKIDKSNQSAFAEALKAIRKQIGIEIRNVHESNEISAYNSALSAGHKI 120
  |||
DB 61 KLRVLIIDKSKIDKSNQSAFAEALKAIRKQIGIEIRNVHESNEISAYNSALSAGHKI 120
  |||
QY 121 WVINDEPRLSIFQYIDAGREELFRNQIKIQTGDIETETKWEYSLEFNKESAFITGY 180
  |||
DB 121 WVLNGFABUSKQYIDAGREELFRNQIKIQTGDIETETKWEYSLEFNKESAFITGY 180
  |||
QY 181 ATASWISQWESKPPVAVSPGQAFPCVTFNDEFAKGIYYNQKHFSSKIYHTSPVKIDS 240
  |||
DB 181 ATASWISQWESKPPVAVSPGQAFPCVTFNDEFAKGIYYNQKHFSSKIYHTSPVKIDS 240
  |||

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[illegible]

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|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|
| 1 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 | | | | | | | | | | | | | | | | | | | |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 1 | 2 | 3 | 4 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE ABC TRANSPORTER XYLOSE-BINDING LIPOPROTEIN.
 GN MYP9_3460.
 OS Mycoplasma pulmonis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes.
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBL_taxID-2107;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN NAB-CTIP;
 RX MEDLINE 21267165; PubMed 11354084;
 RA Chombari L., Hollig R., Ferris S., Barbe V., Samson D., Galisson F.,
 KA Moszer I., Dybiedz K., Wrzblewski J., Viari A., Porcha E.P.C.,
 RA Blanchard A.;
 RT "The complete genome sequence of the murine respiratory pathogen
 RT Mycoplasma pulmonis.";
 RL Nucleic Acids Res. 29:2145-2153(2001).
 DR EMBL: AL445564; CAC14519.1;
 DR MYP9_3460;
 DR InterPro: IPR004760; Bmp.
 DR Pfam: PF02608; Bmp; 1.
 KW Complete proteome.
 FT CHAIN 1 23 465
 SQ SEQUENCE 465 AA, 51149 MW, 67454482680614.0RC64.

QUERY MATCH 21.18, Score 412, DR 19, Length 461.
 Best Local Similarity 30.18; Prod. No: 49619;
 Matches 145; Conservation 94; MisMatches 17; Indels 84; Gaps 21.
 QY 1 MPESEFLLTATATA LEAVAVSTGR 145433 LEEDERKYLTH 17
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 1 MPESEFLLTATATA LEAVAVSTGR 145433 LEEDERKYLTH 17
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 48 ANKQVAVKRAFLKPVVITTEDEKLESEN,SAFEALPAIR 145433 LEEDERKYLTH 17
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 57 KIVNKPFAZLELQVWLTALGRLEHRSIENLYLSSEFLLEQVFAKYSQRLAFNG 116
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 101 PDSRNP PAVYQFASACHPKQWVNTQKQNSIPQY; TAEHETIPKRI 159
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 117 BKTONYNSAVDFE,ENYVALAGCYTWLSTPQCNLEENLEENLEENLEENLEENLEEN 176
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 150 LQDQDPTQYF; WYVQAGNPTSAFTQYVALAGW,PIE; PUSPFWASFPQGA 203
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DE 177 LQVWALAGW,PIE; PUSPFWASFPQGA 203
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 294 PPAVTTNNHAKTLYVNR; HESSEKQHSISIVLELQELATLEMAQV,KNVLSSE 259
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 297 PAVTTEPPTTELDANSEALAKARAVELV,SEELV,LEELV,HAVERLAVSVNVLV 295
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 360 PAIVKPMHVLEAVAGATTEVFLANF; GAYVLAVV,LEOM; LEDEPTELSVL 312
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 296 KSTIS LEVAGTEFVAVV,VERLELSELELV,KNVLSSELEENLEENLEENLEEN 349
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 403 KPIQAVVETHELEPTEFPAV,VEFPA,FWSEHPELEETW,-----VAVNHSSE 402
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 450 FRIATVLE,LEELV,LEELV,LEELV,LEELV,LEELV,LEELV,LEELV,LEELV 402
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 403 KPIQAVVETHELEPTEFPAV,VEFPA,FWSEHPELEETW,-----VAVNHSSE 402
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 403 KPIQAVVETHELEPTEFPAV,VEFPA,FWSEHPELEETW,-----VAVNHSSE 402
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 424 NR 425
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 454 NR 455

RESULT 11
 Q9X775
 ID Q9X775 PRELIMINARY; PRI: 465 AA.
 AC Q9X775
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE P48 MEMBRANE LIPOPROTEIN PRECURSOR.
 GN P48.
 OS Mycoplasma aequaliae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes.
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBL_taxID-2110;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN M7;
 RX MEDLINE 20902629; PubMed 19531294;
 RA Rosati S., Pozzi S., Robino P., Montinaro B., Conti A., Fadda M.,
 RA Pittan M.;
 RT "P48 major surface antigen of Mycoplasma aequaliae is homologous to a
 RT major product of Mycoplasma fermentans and belongs to a selected family
 RT of bacterial lipoproteins.";
 RL Infect. Immun. 67:6213-6216(1999).
 DR EMBL: A132423; CAB43718.1;
 DR InterPro: IPR004760; Bmp.
 DR Pfam: PF02608; Bmp; 1.
 KW Signal; Lipoprotein.
 FT SIGNAL 1 22
 FT CHAIN 23 465
 SQ SEQUENCE 465 AA, 51149 MW, 6045448060496.0RC64.

QUERY MATCH 20.28, Score 412, DR 21, Length 465;
 Best Local Similarity 28.68; Prod. No: 70-18;
 Matches 111; Conservation 90; MisMatches 12; Indels 80; Gaps 17.
 QY 1 MPESEFLLTATATA LEAVAVSTGR 145433 LEEDERKYLTH 17
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 1 MPESEFLLTATATA LEAVAVSTGR 145433 LEEDERKYLTH 17
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 48 ANKQVAVKRAFLKPVVITTEDEKLESEN,SAFEALPAIR 145433 LEEDERKYLTH 17
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 57 KIVNKPFAZLELQVWLTALGRLEHRSIENLYLSSEFLLEQVFAKYSQRLAFNG 116
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 101 PDSRNP PAVYQFASACHPKQWVNTQKQNSIPQY; TAEHETIPKRI 159
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 117 BKTONYNSAVDFE,ENYVALAGCYTWLSTPQCNLEENLEENLEENLEENLEENLEEN 176
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 150 LQDQDPTQYF; WYVQAGNPTSAFTQYVALAGW,PIE; PUSPFWASFPQGA 203
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DE 177 LQVWALAGW,PIE; PUSPFWASFPQGA 203
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 294 PPAVTTNNHAKTLYVNR; HESSEKQHSISIVLELQELATLEMAQV,KNVLSSE 259
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 297 PAVTTEPPTTELDANSEALAKARAVELV,SEELV,LEELV,HAVERLAVSVNVLV 295
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 360 PAIVKPMHVLEAVAGATTEVFLANF; GAYVLAVV,LEOM; LEDEPTELSVL 312
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 296 KSTIS LEVAGTEFVAVV,VERLELSELELV,KNVLSSELEENLEENLEENLEEN 349
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 403 KPIQAVVETHELEPTEFPAV,VEFPA,FWSEHPELEETW,-----VAVNHSSE 402
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 450 FRIATVLE,LEELV,LEELV,LEELV,LEELV,LEELV,LEELV,LEELV,LEELV 402
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 403 KPIQAVVETHELEPTEFPAV,VEFPA,FWSEHPELEETW,-----VAVNHSSE 402
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 403 KPIQAVVETHELEPTEFPAV,VEFPA,FWSEHPELEETW,-----VAVNHSSE 402
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 424 NR 425
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 DB 454 NR 455

RESULT 12
 Q48902
 ID Q48902 PRELIMINARY; PRI: 457 AA.
 AC Q48902
 DT 01-NOV-1999 (TrEMBLrel. 01, Created)
 DT 01-NOV-1999 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE AG 243-5 PROTEIN PRECURSOR.
 OS Mycoplasma arginini.

RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Kadane D.,
 RA Holtzapfel E., Kozak M., Wall A.M., Bhatnagar K.P., Hansen S.L.,
 RA McDonald L.A., Feldblyum T.V., Anisotti S., Dickinson T., Hickey E.K.,
 RA Holt L.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Donnelly B.A., Morrison D.A., Hollnash S.K., Fraser C.M.,
 RT "Complete genome sequence of a virulent isolate of *Streptococcus*
 RT *pneumoniae*."
 RL Sequence 293,498 506 (2001).
 DK EMBL: AE007498; AKK4475.1;
 DK TIGR: SP0845;
 BK InterPro: IPK00114; Adenylsucc_synth.
 DK InterPro: IPK004760; Bmp.
 DK InterPro: IPK00217; tubulin.
 DK Pfam: PF02608; Bmp; 1.
 DK PROSITE: PS00227; TUBULIN; INKRP-WL.1.
 KW Complete proteome.
 SQ SEQUENCE 450 AA: 40746 MW: 40767477501659 CRG64;

Query Match 10.48; Score 225; DB 16; Length 350;
 Best local similarity 25.48; Prod. No. 150-05;
 Matches 97; Conservative 57; Mismatches 151; Indels 78; Gaps 15;
 QY 1 MKKSKKTHLSPDAATPAVAVSNGRPGRHLEKRTLSKYTTNANCKAVVMAELL 60
 DB 1 MKKSKKTHLSPDAATPAVAVSNGRPGRHLEKRTLSKYTTNANCKAVVMAELL 60
 QY 61 KLEVLVLDKDKTKRSKSAALALAKDKGGLGLRN--VLEDSHESAYASALSA 116
 DB 61 KLEVLVLDKDKTKRSKSAALALAKDKGGLGLRN--VLEDSHESAYASALSA 116
 QY 47 KTKAIVVLDKDKTKRSKSAALALAKDKGGLGLRN--VLEDSHESAYASALSA 96
 DB 47 KTKAIVVLDKDKTKRSKSAALALAKDKGGLGLRN--VLEDSHESAYASALSA 96
 QY 117 GRKRWLN--GVKESKQVLEDAUPTVLEQVLEKRTLSKYTTNANCKAVVMAELL 175
 DB 117 GRKRWLN--GVKESKQVLEDAUPTVLEQVLEKRTLSKYTTNANCKAVVMAELL 175
 QY 97 (SYNLITVAVLNNV)--DAKKEKTVGVLL--LVKDKKRVASVTEADRESG 149
 DB 97 (SYNLITVAVLNNV)--DAKKEKTVGVLL--LVKDKKRVASVTEADRESG 149
 QY 176 PTTVYAIASWISPADESKRVVSPGGGAFPGVITTFNPFAGKILLYNQRKSKIVHTSP 235
 DB 176 PTTVYAIASWISPADESKRVVSPGGGAFPGVITTFNPFAGKILLYNQRKSKIVHTSP 235
 QY 150 VIAVA--K--FTTFKAVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 195
 DB 150 VIAVA--K--FTTFKAVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 195
 QY 246 VLLSSEFVGF--FNTVIRHVLSTAVKRYNPHVILSVAGIAVETVPLANPQ-- 289
 DB 246 VLLSSEFVGF--FNTVIRHVLSTAVKRYNPHVILSVAGIAVETVPLANPQ-- 289
 QY 196 VQVYVASEGLAAKRIIAAAYAAAVVQ--VAGGIGAGVFAFASLNSPENEK 252
 DB 196 VQVYVASEGLAAKRIIAAAYAAAVVQ--VAGGIGAGVFAFASLNSPENEK 252
 QY 290 --YVGVSDQ--GMLDKRP--ILTSVLKHPKAAVVEILLIDKEEGYK-- 346
 DB 290 --YVGVSDQ--GMLDKRP--ILTSVLKHPKAAVVEILLIDKEEGYK-- 346
 QY 253 VVVIGVDRDQAFGKYTSKCKESNFIIVSTIKQ--VILLVKTLSNKAERGEEFGGLV 408
 DB 253 VVVIGVDRDQAFGKYTSKCKESNFIIVSTIKQ--VILLVKTLSNKAERGEEFGGLV 408
 QY 447 --YVGVSDQ--GMLDKRP--ILTSVLKHPKAAVVEILLIDKEEGYK-- 488
 DB 447 --YVGVSDQ--GMLDKRP--ILTSVLKHPKAAVVEILLIDKEEGYK-- 488
 QY 409 VVYGVSDQ--GMLDKRP--ILTSVLKHPKAAVVEILLIDKEEGYK-- 456
 DB 409 VVYGVSDQ--GMLDKRP--ILTSVLKHPKAAVVEILLIDKEEGYK-- 456

RESULT 15
 QYAK41
 ID QYAK41 PRELIMINARY; PKT: 448 AA.
 AC QYAK41;
 DT 01-JUN-2001 (16MAYrel. 17, created)
 BL 01-JUN-2001 (16MAYrel. 17, last sequence update)
 DT 01-OCT-2001 (16MAYrel. 18, last annotation update)
 DE PUTATIVE LIPOPROTEIN.
 GN 250K8.11.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID:1402;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-A4(2);
 RA Sequer K., Barris D.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 RN 12
 RP SEQUENCE FROM N.A.
 RC STRAIN-A4(2);

RA Cardeno A.M., Parkhill J., Bartell B.G., Rajandream M.A.,
 S. Jambou A. (et al.) 2001. The genome of *Streptomyces*
 RP SEQUENCE FROM N.A.
 RC STRAIN-A4(2);
 RX MEDLINE:97000351; PubMed 8843446;
 KA Redenbach M., Kleser H.M., Denapaire D., Eichner A., Gullum J.,
 KA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb *Streptomyces coelicolor* A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 DK EMBL: AL589164; CA33050.1;
 DK InterPro: IPK004760; Bmp.
 DK Pfam: PF02608; Bmp; 1.
 KW Lipoprotein.
 SQ SEQUENCE 448 AA: 36071 MW: 4367A390D5E7B86F CRG64;

Query Match 9.78; Score 212; DB 2; Length 348;
 Best local similarity 24.98; Prod. No. 8.6e-05;
 Matches 107; Conservative 67; Mismatches 144; Indels 90; Gaps 19;
 QY 1 MKKSKKTHLSPDAATPAVAVSNGRPGRHLEKRTLSKYTTNANCKAVVMAELL 58
 DB 1 MKKSKKTHLSPDAATPAVAVSNGRPGRHLEKRTLSKYTTNANCKAVVMAELL 58
 QY 1 MKKSKKTHLSPDAATPAVAVSNGRPGRHLEKRTLSKYTTNANCKAVVMAELL 42
 DB 1 MKKSKKTHLSPDAATPAVAVSNGRPGRHLEKRTLSKYTTNANCKAVVMAELL 42
 QY 59 LKPLKVLTLSPSTNCAFTAFALPKATLPTPRVPS--SNPLAYRSA 114
 DB 59 LKPLKVLTLSPSTNCAFTAFALPKATLPTPRVPS--SNPLAYRSA 114
 QY 43 -----IATVGGKGGQSDNDAAYAGLEQAKKEFGYVADVEPTGDTDAKFORLSH 95
 DB 43 -----IATVGGKGGQSDNDAAYAGLEQAKKEFGYVADVEPTGDTDAKFORLSH 95
 QY 114 LSAGKFWV--GK--GK--GK--GK--GK--GK--GK--GK--GK--GK--GK--GK-- 169
 DB 114 LSAGKFWV--GK--GK--GK--GK--GK--GK--GK--GK--GK--GK--GK-- 169
 QY 96 AKQYNNVAVVGLGVAYASAMKNVAAKYDT-----TGLVLAATLEAKNVALLVF 144
 DB 96 AKQYNNVAVVGLGVAYASAMKNVAAKYDT-----TGLVLAATLEAKNVALLVF 144
 QY 170 NIKESATTTVYIASWISPADESKRVVSPGGGAFPGVITTFNPFAGKILLYNQRKSK 229
 DB 170 NIKESATTTVYIASWISPADESKRVVSPGGGAFPGVITTFNPFAGKILLYNQRKSK 229
 QY 145 NEQFASVLAGVAAA-----KSTRINIVGVGVGVGVGVGVGVGVGVGVGVGVGV 199
 DB 145 NEQFASVLAGVAAA-----KSTRINIVGVGVGVGVGVGVGVGVGVGVGVGVGV 199
 QY 239 LYHPSFVLDGTTAGTCKRMTV--NRVLSSTPAVKYNPHVILSVAGIAVETVPLANPQ 289
 DB 239 LYHPSFVLDGTTAGTCKRMTV--NRVLSSTPAVKYNPHVILSVAGIAVETVPLANPQ 289
 QY 200 QY1QTAF--PQV--PQV--PQV--PQV--PQV--PQV--PQV--PQV--PQV--PQV-- 252
 DB 200 QY1QTAF--PQV--PQV--PQV--PQV--PQV--PQV--PQV--PQV--PQV-- 252
 QY 200 VVI--V--G--G--G--G--G--G--G--G--G--G--G--G--G--G--G--G-- 443
 DB 200 VVI--V--G--G--G--G--G--G--G--G--G--G--G--G--G--G--G--G-- 443
 QY 253 WAIIVSDQ--GMLDKRP--ILTSVLKHPKAAVVEILLIDKEEGYK-- 404
 DB 253 WAIIVSDQ--GMLDKRP--ILTSVLKHPKAAVVEILLIDKEEGYK-- 404
 QY 444 ADKFWSGKGLKAWGVAFNR--FSNTEPQAKINNKATFAKMEKE 488
 DB 444 ADKFWSGKGLKAWGVAFNR--FSNTEPQAKINNKATFAKMEKE 488
 QY 405 -----GDLASGEVGLSSNPKFAADAK-----LGAATASAKE 456
 DB 405 -----GDLASGEVGLSSNPKFAADAK-----LGAATASAKE 456

Search completed: July 23, 2002, 14:43:46
 Job time: 134 sec

031362;
 DI 15-DEC-1998 (Rev. 37, Created)
 DI 15-DEC-1998 (Rev. 37, Last sequence update)
 DI 15-DEC-1998 (Rev. 37, Last annotation update)
 DE Basic membrane protein B precursor.
 GN BMPB.
 OS Borrelia burgdorferi.
 OS Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_taxid:29519;
 RN [1]
 RP SEQUENCE FROM N.A.
 FC STRAIN PBI;
 FC MEDLINE:98010210; PubMed:9450727;
 RA Roessler J., Hauser B., Wilske B.,
 RA "Reactivity of BspA (239) among European isolates of Borrelia
 RA burgdorferi sensu lato and influence of interspecies variability on
 RA serodiagnosis.";
 RI J. Clin. Microbiol., 45:2752-2758(1997).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 (Probable).
 CC -1- SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS.
 CC
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 DR EMBL: X81518; CAA57249.1;
 DR InterPro: IPR004760; Bmp.
 DR Pfam: PF02609; Bmp; 1.
 DR ProSITE: PS00018; PROKAR_LIPOPROTEIN; 1.
 KW Membrane; Lipoprotein; Signal.
 FT SIGNAL 1 14 PROBABLE.
 FT CHAIN 15 44 BASIC MEMBRANE PROTEIN B.
 FT LIPID 15 15 N-ACYL DIGLYCERIDE (PROBABLE).
 SQ SEQUENCE 441 AA: 37246 MW: 4428069D0C9A CR664;
 Query Match 7.08; Score 169; DB 1; Length 341;
 Best Local Similarity 21.58; Pred. No. 0.0084;
 Matches 92; Conservative 92; Mismatches 169; Indels 80; Gaps 15;
 QY 17 TIPAAVAVV...GRHSNHLFFLELLEFETLTGAKFEAVVHPELEFTEV;159 FF 74
 DB 7 TGLHLLSTAGNTERSSS-----KIKLSMLVD-GVLD 49
 QY 75 DESTRSSSEELAKAPLGLLETRV LFGSELSAY KSLASWDRKWLWLETF 127
 DB 40 DKSTSSSAREALKEELFEELFENLTKVLSAAAGVLSVYSGTINIKRSGGLWVGND 99
 QY 129 EQQTEKLYLAHHVTEFQKLTQDQ DTEFEYKWEVSLNIPESAVTQYALIA 183
 DB 100 IDANLS-----VSLNPKLSGLIDVYVSHVGLP KKLGVVERIQCAFLADYIAA 151
 QY 184 SWLSGLLESEV VAAQGLALGV LILHLSALSLVYDKEKSKINIEFVELLS 213
 DB 152 EFAVSEFTLELSEAVSEAVALEFV LIAAGVAAV LILVSLVNGEFGVH 203
 QY 241 QTTATEKRRVTRVSSSTFANKYHIVHLEVAQVATFETVLANKQGVGVGVSDQM 400
 DB 204 GPALANRYAPLHLEL-----HPMAVAGSVLEAFETVGVVGVSAFAGVGR 263
 QY 401 LQDKRHLISWIKHKGAVVETLILLEFEFGEYKPVVWVLEKAKKWSHFEQKRW 358
 DB 263 LAPEN-FHLSVKNQVALVATSEVLEKRNWLEKE TIGQCLQGVVGLSHRHFPEY 409
 QY 469 LQVAPRHVTRFTEAKINRE LFEATKM 385
 DB 410 LKVTERTVNEELIVPNHSEVETFTQIKL 441

RESULT 12
 BMPB_BORBU
 ID BMPB_BORBU STANDARD: PRT: 441 AA.
 AC Q44743;
 DI 15-DEC-1998 (Rev. 37, Created)
 DI 15-DEC-1998 (Rev. 37, Last sequence update)
 DI 16-DEC-2001 (Rev. 40, Last annotation update)
 DE Basic membrane protein B precursor.
 GN BMPB OR BHO385.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OS Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_taxid:139;
 RN [1]
 RP SEQUENCE FROM N.A.
 FC STRAIN JDI;
 FC MEDLINE:96178617; PubMed:8606088;
 FC Ramamoorthy R., Powell L.L., Philipp M.T.;
 FC "Molecular characterization, genomic arrangement, and expression of
 FC bmpB, a new member of the bmp class of genes encoding membrane
 FC proteins of Borrelia burgdorferi.";
 RI Infect. Immun., 64:1259-1264(1996).
 CC -1- SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS.
 CC
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.isb-sib.ch) or
 CC or send an email to license@sib-sib.ch).
 DR EMBL: U45450; AAC13984.1;
 DR EMBL: AK001144; AAB91505.1;
 DR TIGR: BHO385;
 DR InterPro: IPR003760; Bmp.
 DR Pfam: PF02608; Bmp; 1.
 DR ProSITE: PS00018; PROKAR_LIPOPROTEIN; 1.
 KW Membrane; Lipoprotein; Signal; Complete proteome.
 FT SIGNAL 1 16 PROBABLE.
 FT CHAIN 15 43 BASIC MEMBRANE PROTEIN B.
 FT LIPID 17 17 N-ACYL DIGLYCERIDE (PROBABLE).
 SQ SEQUENCE 441 AA: 47163 MW: 646664691A91D5 CR664;
 Query Match 7.08; Score 154; DB 1; Length 341;
 Best Local Similarity 23.28; Pred. No. 0.0074;
 Matches 92; Conservative 92; Mismatches 152; Indels 98; Gaps 20;
 QY 22 VSGNNSRSEMLTEKELEKYLLEARPEAVVFNATLEFTEFVLEFTEKTFKPEKSA 92
 DB 15 VASSSSDU-----GSESAKVSLV
 QY 84 FFLAKATKQVLEHIVRVSS-----STVATSSALSAKRWLETFEATV 142
 DB 46 SKATKKE KAGDNGGLKASIGREYLGAGLELSSRSR LAGG GFEESDIL 98

[illegible]

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QM protein protein search, using sw model

Run on: July 23, 2002, 11:37:17, Search time 20:47:35 seconds
(without alignments)
1970.591 Million cell updates/sec

Title: US-09-601-371_2

Perfect score: 2189
Sequence: 1 MF2FFHLLSLFAMILFA.....HVFSEGLAIALNPAAE 129

Scoring table: BLASTM62

Gapop 10.0, Gapext 0.5

Searched: 28438 seqs, 9608934 residues

Total number of hits satisfying chosen parameters: 28438

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processed: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
|------------|-------|-------|--------|----|--------------------|
| 1 | 462 | 21.1 | 461 | 2 | Protein |
| 2 | 225 | 10.3 | 450 | 2 | G95097 |
| 3 | 220.5 | 10.1 | 677 | 2 | Lipoprotein [impor |
| 4 | 213 | 9.7 | 473 | 2 | probable lipoprote |
| 5 | 207.5 | 9.5 | 591 | 2 | conserved hypotet |
| 6 | 204.5 | 9.3 | 525 | 2 | membrane lipoprote |
| 7 | 203 | 9.3 | 439 | 2 | conserved hypotet |
| 8 | 201.5 | 9.2 | 357 | 2 | probable lipoprote |
| 9 | 196.7 | 8.7 | 375 | 2 | membrane lipoprote |
| 10 | 197 | 9.0 | 441 | 2 | basic membrane lip |
| 11 | 192 | 8.9 | 450 | 2 | hypothetical memb |
| 12 | 190.5 | 8.7 | 624 | 2 | ABC transporter (1 |
| 13 | 187 | 8.5 | 450 | 1 | C99004 |
| 14 | 180.5 | 8.2 | 457 | 2 | AD1248 |
| 15 | 178.5 | 8.2 | 357 | 2 | AB1510 |
| 16 | 173 | 7.9 | 459 | 2 | F72418 |
| 17 | 155.5 | 7.1 | 360 | 2 | H73157 |
| 18 | 153 | 7.0 | 447 | 2 | B97374 |
| 19 | 153 | 7.0 | 377 | 2 | AB1571 |
| 20 | 152 | 6.9 | 470 | 2 | F72494 |
| 21 | 151 | 6.9 | 665 | 1 | D61203 |
| 22 | 144 | 6.6 | 322 | 2 | F94246 |
| 23 | 142.5 | 6.5 | 353 | 2 | G70137 |
| 24 | 140.5 | 6.4 | 494 | 2 | G75161 |
| 25 | 138 | 6.3 | 624 | 2 | F62003 |
| 26 | 137 | 6.3 | 539 | 2 | D82886 |
| 27 | 136.5 | 6.2 | 1225 | 2 | G53591 |
| 28 | 134.5 | 6.1 | 805 | 2 | G82884 |
| 29 | 134.5 | 6.1 | 2401 | 2 | T24071 |

ALIGNMENTS

RESULTS

1

690555

ABC transporter, see binding lip protein [impor] Mycoplasma pulmonis (strain H

01) Species: Mycoplasma pulmonis

Database: 24 May 2001 [us protein_v18] v. 24-May-2 1:10:01 Update us-Aug-2001

Accession: B00055

Reinhardt, L., Reddy, R., Fortis, S., Barto, V., Samson, J., Nilsson, P., Moser, N

Nucleic Acids Res. 29, 2135-2144, 2001

Abstract: The complete genome sequence of the model respiratory pathogen Mycoplasma p

Accession number: AF121212

Accession: B00055

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Accession: B00055

Best local similarity: 25.5%, Prod. No. 0.00042
 Matches: 42, Conservation: 44, Mismatches: 152, Indels: 82, Gaps: 8

 QY 5 PFLILGCTAAITAVAGVGRHLSGISTFLEISPAITLISARCTGVVMAHLKRP 64
 II III III III III III III III III III III III III III III III
 DB 2 KPVVIAVMAIASVAVIAVPSHMAAGSVAZTD-----LKA 39

 QY 65 VLTIPKIPKSTNSCAPITALA-----LNGTFLITNSVPSSNPSAYNSALSACH 118
 III III III III III III III III III III III III III III III III
 DB 40 ALVTEIGVNDSPNSAMPGLQSWKFNPKKGLAYVYVAGSASADYVTHSAFQCY 99

 QY 119 FQWNLNPFHQSDEQVLAHPELEENQSTFICIDHPIETEEKWPSLOFNKESAFIT 178
 III III III III III III III III III III III III III III III III
 DB 100 KALFELGHSGL-----DALSAAGNRHPSRLVIVMSVLEPKRVASATPAINSAVLA 152

 QY 179 GYAIASWLTGQREVAAGTGAITVATGSAAPLQVQSGDQVQVYHSTVAV 248
 III III III III III III III III III III III III III III III III
 DB 153 GVAAAFAKINATGSLQMSGVITFELKSLFACAGSNVDFVAVAGSFSVA 207

 QY 249 DSGTACHPHIVRHVIGSTFAVETHPVIVLISVAGHATTEVELARQGVYVI 292
 III III III III III III III III III III III III III III III III
 DB 208 APTPTIATAMQVATVAVVATATV-----GTNGVQAFATGTHHAFVWVI 259

 QY 293 GVDSPQWY-----QVPHPTSTWPHHPAAVPTETITLIPKPPYKIVVKKRVA 344
 III III III III III III III III III III III III III III III III
 DB 257 GVPSTQVHVPYFKEFQVSHVAVSTQVAVVAVP-----VATLPTIF 294

 QY 345 DKW 349
 III III
 DB 300 DKF 303

 RESULT 12
 DB2944
 Hypothetical membrane lipoprotein U0016 [imported] - Ureaplasma urealyticum
 C>Date: 18 Aug 2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: DB2944
 R:Glass, J. J., Letkowski, E. J., Glass, J. S., Bolner, C. F., & Cassell, C. H.
 submitted to GenBank, February 2000
 A:Description: The complete sequence of Ureaplasma urealyticum. Amino acid sequence of a 349
 A:Reference number: AB2870
 A:Accession: DB2944
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1 524 (GLA)
 A:Cross references: GB:AF002131; GB:AL222994; NID:46999967; FIDR:AAF0421.1; G330462001
 A:Experimental source: strain 2, L37041
 C:Genetics:
 A:Gene: U0016
 C:Superfamily: ABC transporter yuN

Query Match: 9.7%, Score 190.5, DB 1, Length 524
 Best local similarity: 24.1%, Prod. No. 0.00042
 Matches: 120, Conservation: 103, Mismatches: 199, Indels: 125, Gaps: 22

 QY 1 MPPS-----PFLITLITAAITAVAGVGRHLSGISTFLEISPAITLISARCTGVVMAHLKRP 56
 III III III III III III III III III III III III III III III III
 DB 1 MKKSKTRKFKLLASLAGVVLISVAAIAAGSN-----KIDSK-TNKIRNVISK- 50

 QY 57 APTPTIATAMQVATVAVVATATV-----GTNGVQAFATGTHHAFVWVI 116
 III III III III III III III III III III III III III III III III
 DB 51 ---LSEDFYAKDQ--HD-----SLGVRHYVNSLYDD 78

 QY 117 GHPVAVKLPKQVIFVYHAMPETLQVQV-----LTPKFWVQVAGVMAFPAV 176
 III III III III III III III III III III III III III III III III
 DB 79 GAPMLGLISLSSHPDREYFSSSSSKRLSAVLLIDKESCTWQKPLASVSPVQQAAP 137

 QY 177 ITGYAIASWSEQD-----FSKRVVASFGGAGVGVITENEGFAKGLLYYNOKHK----- 226
 III III III III III III III III III III III III III III III III
 DB 148 LIGIAAAVYLNAGOTFAAGCKLWGGVYHHEFTSTSTETQDFFELGVWANEKIKTFEIN 197

QY 227 SSKLYHTSPVKLPSSTAG-----PKMTVYNNVISTDAVVPYNDIVLISVAG 275
 III III III III III III III III III III III III III III III III
 DB 198 QEANGSFEKMMVVCATFAGVYVAGSSTETETEGATHHETELTEPAD-----VILPVA 251

 QY 276 PAT---FEIVELAMQVYVGVDSQGM-----TQKQRIILTSVIFIKQAV 319
 III III III III III III III III III III III III III III III III
 DB 252 POTHAIUSVSRATDSVAGVLAJAGVAVVHEKSTCKVHEGKILLESIVKAVDIA- 310

 QY 320 YEILLEDILKEEYKRYVYVVEKFAKESKSHFGLDFFKLVGAEN---HPSK-----FE 371
 III III III III III III III III III III III III III III III III
 DB 311 ---MKGATFNASKCAQLINDIRKDAYKLGTHHATASIKSTVYVHTLVLSHAGVAVY 467

 QY 472 QAFIRKRLALATBEFL-----LVVLRSSAKKCHDRAVS 413
 III III III III III III III III III III III III III III III III
 DB 368 AAFACGLFAAGAGVAVGAG-----LITFLTGLDITGLTAAATLVWFPSSTPPE 426

 QY 414 ERGLATISA---INRAAR 428
 III III III III III III III III III III III III III III III III
 DB 427 E-DKLLAGREVYNESDK 443

 RESULT 13
 C70009
 ABC transporter (lipoprotein) homolog yuN - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 18 Sep 1999 #sequence_revision 16-Sep-1999 #text_change 21-Sep-2000
 C:Accession: C70009
 R:Kunst, F., Ogasawara, N., Masters, J., Albertini, A. M., Allcoli, G., Arzvedo, V., Ber
 C:Bron, S., Broillet, S., Bruschi, C. V., Caldwell, B., Capuano, V., Carter, N. M.,
 A:Erlich, S. D., Emerson, P. T., Entian, K. D., Errington, J., Fabrizi, C., Ferrari,
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Gallizzi, A., Gal
 lech, J., Harwood, C. R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M
 Koeltter, P., Koningsstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardino
 A:Authors: Lauber, J., Lazarovic, V., Lee, S. M., Levine, A., Lin, H., Masada, S., Mau
 Y., K., Ogawa, K., Oikawa, A., Oudena, R., Park, S. H., Parro, V., Pohl, L. M., Porteto
 Pleguez, M., Pivetta, C., Pocha, F., Poche, P., Ponce, M., Sadava, Y., Sato, T., Soani
 A:Authors: Schleicher, S., Schuetter, R., Skoffone, F., Sekiguchi, J., Skokowska, A., Se
 akouchi, M., Tanakashi, A., Tanaka, T., Tepest, A., Taniuchi, A., Tazaki, Y., Uchiya
 T., Wilfert, P., Wipat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, K., Yoshida
 A:Authors: Y. S. Iwano, B. F. Winstein, F. Yoshikawa, H. Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
 A:Reference number: A69580; MIMD:98044033
 A:Accession: C70009
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-250 (PUN)
 A:Cross references: GB:G99129; GB:AF099126; NID:42645614; PIDR:CAH1514.1; FID:426356
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yuN
 C:Superfamily: ABC transporter yuN

Query Match: 9.5%, Score 187, DB 1, Length 350
 Best local similarity: 32.4%, Prod. No. 0.00029
 Matches: 91, Conservation: 61, Mismatches: 145, Indels: 116, Gaps: 17

 QY 24 SCRRPESHUSLPELEETETINAPVAVVAGVGRHLSGISTFLEISPAITLISARCTGVVMAHLKRP 83
 III III III III III III III III III III III III III III III III
 DB 13 AGNSERSAGSGEGRN-----KPSVAVTAVGVVGRSPNSAW 51

 QY 84 EAKKALHPKGLIEN-----NVPSRPSPSAVNSAI-SWDRTPVNI 124
 III III III III III III III III III III III III III III III III
 DB 52 EALALDELPELEGRVAVVAGVGRHLSGISTFLEISPAITLISARCTGVVMAHLKRP 99

 QY 125 GPKHQQSIRVYIAHRELEENQIKLIGIHPIETEEKWPSLOFNKESAFITGYAIAS 184
 III III III III III III III III III III III III III III III III
 DB 100 GYLMEDSISEAD-----QPKNTINPAIIVAVVDKIN--VASITFEKSGSLVGVMAA- 150

 QY 195 WLSRDEDSKRVVASFGGAGVGVITENEGFAKGLLYYNOKHKSKLYHTSPVKLPSSTAG 244
 III III III III III III III III III III III III III III III III
 DB 151 -LSKSGK---TGVPQGMSEFLKKFELVGFPAVAVNPKRVAVVGVYVAGVMAHLKRP 206



GenCore version 4.5
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OM protein protein search, using sw model

Run on: July 23, 2002, 11:29:42 : Search time 11.56 seconds
(without alignments)
1506,801 Million cell updates/sec

Title: US-09-601-371-2
Perfect score: 2189
Sequence: 1 MEKSKETLLEKLSF-AAIQA.....LAVSEEDIA-IAIRAAK 429

Scoring table: BL/SDM62
Gapop 10.0 : Gapext 0.5

Searched: 747574 seqs, 11167796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listed first 45 summaries

Database : A_GenSeq_032802:*

| Rank | Seq ID | Score | Length | DB ID | Description |
|------|-----------|-------|--------|-------|-------------|
| 1 | AA1000001 | 2189 | 100.0 | 429 | 20 AAY5492 |
| 2 | AA1000002 | 2062 | 95.4 | 129 | 19 AAW2275 |
| 3 | AA1000003 | 868 | 49.7 | 166 | 22 AAY7352 |
| 4 | AA1000004 | 419 | 19.1 | 453 | 14 AAR40856 |
| 5 | AA1000005 | 403.5 | 18.4 | 448 | 10 AAP93343 |
| 6 | AA1000006 | 396.5 | 18.3 | 442 | 16 AAR67582 |
| 7 | AA1000007 | 294.5 | 19.5 | 451 | 22 AAY01855 |
| 8 | AA1000008 | 468 | 16.8 | 424 | 22 AAY01860 |
| 9 | AA1000009 | 252 | 11.5 | 429 | 22 AAY9289 |
| 10 | AA1000010 | 225 | 10.3 | 351 | 21 AAY81632 |
| 11 | AA1000011 | 205.5 | 9.4 | 328 | 19 AAW55066 |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
|------------|-------|-------|--------|-------------|--------------------|
| 1 | 2189 | 100.0 | 429 | 20 AAY5492 | Inflammatory cytok |
| 2 | 2062 | 95.4 | 129 | 19 AAW2275 | Membrane protein H |
| 3 | 868 | 49.7 | 166 | 22 AAY7352 | Interleukin X (IL |
| 4 | 419 | 19.1 | 453 | 14 AAR40856 | 4 kb regression as |
| 5 | 403.5 | 18.4 | 448 | 10 AAP93343 | Gene encoding the |
| 6 | 396.5 | 18.3 | 442 | 16 AAR67582 | Cancer metastasis |
| 7 | 294.5 | 19.5 | 451 | 22 AAY01855 | Mycoplasma hyopneu |
| 8 | 468 | 16.8 | 424 | 22 AAY01860 | Mycoplasma hyopneu |
| 9 | 252 | 11.5 | 429 | 22 AAY9289 | Propionibacterium |
| 10 | 225 | 10.3 | 351 | 21 AAY81632 | Streptococcus pneu |
| 11 | 205.5 | 9.4 | 328 | 19 AAW55066 | Streptococcus pneu |

| | | | | | |
|----|-------|-----|-----|-------------|--------------------|
| 12 | 204.5 | 9.3 | 440 | 14 AAR31134 | Streptococcus pneu |
| 13 | 203 | 9.3 | 424 | 20 AAY19946 | B. burgdorferi ant |
| 14 | 201 | 9.3 | 429 | 20 AAW61157 | B. burgdorferi ant |
| 15 | 200 | 9.3 | 449 | 20 AAY19984 | B. burgdorferi ant |
| 16 | 195.5 | 8.7 | 341 | 20 AAY19984 | B. burgdorferi ant |
| 17 | 192 | 8.5 | 441 | 19 AAW19960 | B. burgdorferi ant |
| 18 | 187 | 8.2 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 19 | 182 | 8.0 | 441 | 19 AAW19960 | B. burgdorferi ant |
| 20 | 177 | 7.7 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 21 | 175 | 7.6 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 22 | 170 | 7.3 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 23 | 167 | 7.1 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 24 | 163 | 6.9 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 25 | 160 | 6.7 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 26 | 155 | 6.4 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 27 | 151 | 6.2 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 28 | 148 | 6.0 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 29 | 145 | 5.8 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 30 | 142 | 5.6 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 31 | 139 | 5.4 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 32 | 136 | 5.2 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 33 | 133 | 5.0 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 34 | 130 | 4.8 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 35 | 127 | 4.6 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 36 | 124 | 4.4 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 37 | 121 | 4.2 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 38 | 118 | 4.0 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 39 | 115 | 3.8 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 40 | 112 | 3.6 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 41 | 109 | 3.4 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 42 | 106 | 3.2 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 43 | 103 | 3.0 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 44 | 100 | 2.8 | 441 | 20 AAY19984 | B. burgdorferi ant |
| 45 | 97 | 2.6 | 441 | 20 AAY19984 | B. burgdorferi ant |

REFERENCES

RESULT 1
AA1000001

AA1000002

AA1000003

AA1000004

AA1000005

AA1000006

AA1000007

AA1000008

AA1000009

AA1000010

AA1000011

AA1000012

AA1000013

AA1000014

AA1000015

AA1000016

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AA1000168

AA1000169

AA1000170

AA1000171

useful for the treatment of thrombocytopaenia.

| XX SQ | Sequence | 428 AA |
|----------|---|--|
| | Query Match | 100.0%, Score 4289, E3.20, Length 429, |
| | Best Local Similarity | 100.0%, Prod. No. 30-157, |
| | Matches 428/ conservative | 0/ Mismatches 0/ Indels 0/ Gaps |
| QY | 1 MRSKKKIIHISGIAALIDAVAVSSNNPISNLSIFERFISKYTTINAKRGVVKNAELL 60 | |
| DB | 1 MRSKKKIIHISGIAALIDAVAVSSNNPISNLSIFERFISKYTTINAKRGVVKNAELL 60 | |
| QY | 61 PEPVAVSSGILGIFGKFNAGALAAANAGVGLIDAVVLSGRTSNANSLASGRI 120 | |
| DB | 61 PEPVAVSSGILGIFGKFNAGALAAANAGVGLIDAVVLSGRTSNANSLASGRI 120 | |
| QY | 121 WVLRFPRFQVDSIKCYIDAPRERFRRGPKRIKGLIHTLITETKRWYSISGPNIKISATTCY 180 | |
| DB | 121 WVLRFPRFQVDSIKCYIDAPRERFRRGPKRIKGLIHTLITETKRWYSISGPNIKISATTCY 180 | |
| QY | 181 ATASISPSGSSKAVVASFGGSGAPGVVSNENSGAPGVVSNENSGAPGVVSNENSGAPGV 240 | |
| DB | 181 ATASISPSGSSKAVVASFGGSGAPGVVSNENSGAPGVVSNENSGAPGVVSNENSGAPGV 240 | |
| QY | 241 YETAIFPNTVIRNVISSSTAFVKNPWRVIVACVATFETVPIANEGVYIVTSQWGM 300 | |
| DB | 241 YETAIFPNTVIRNVISSSTAFVKNPWRVIVACVATFETVPIANEGVYIVTSQWGM 300 | |
| QY | 301 IQGKIRHITSVIKHILAVYETTLIDITERRFQVGVVGVKPKKAFKWSHPGTPKRWIG 360 | |
| DB | 301 IQGKIRHITSVIKHILAVYETTLIDITERRFQVGVVGVKPKKAFKWSHPGTPKRWIG 360 | |
| QY | 361 VAPNHSSTFEPAPINRPFEAKKMPIDRIVVYDASGKALYGNPKNVSEKAL 420 | |
| DB | 361 VAPNHSSTFEPAPINRPFEAKKMPIDRIVVYDASGKALYGNPKNVSEKAL 420 | |
| QY | 421 GATPPEAP 429 | |
| DB | 421 GATPPEAP 429 | |

| | |
|----------|---|
| RESULT 2 | |
| AAW22727 | |
| ID | AAW22727 standard; Protein: 429 AA. |
| XX | |
| XX | AAW22727; |
| XX | |
| DI | 26-FEB-1998 (first entry) |
| XX | |
| DE | Membrane protein M61Aq. |
| XX | |
| KW | M61Aq; membrane protein; leukemia; treatment. |

| | | | |
|----------|--|---|---------------------|
| FH | | Key | Location/Qualifiers |
| FI | Miso-Difference | 160 | "Encoded by TGA" |
| FI | Miso-Difference | 160 | "Decoded by TGA" |
| FN | SSZ001019713-A1. | | |
| XX | 06-SEP-2001: | | |
| XX | 16-JAN-2001: | 2003US 0760541. | |
| XX | 08-MAR-1994: | 940S-0287487. | |
| XX | 11-FEB-1993: | 940S-0026142. | |
| XX | (BLAZ7) BLAZAR B A. | | |
| XX | (WEBB7) WEBB A C. | | |
| XX | Blazar BA Webb AC. | | |
| XX | 59 Jul 2001 570181764 | | |
| DR | N-P5DB; AAS11796. | | |
| XX | New IL-X polypeptide useful e.g., for enhancing the growth of cells in vitro, for growing primary human B cell cultures to facilitate proliferation of these cell lines, as therapeutics or prophylactics, as molecular weight standards - | | |
| PI | claim 7; page 7; 16pp; English. | | |
| PS | The invention relates to a novel secreted autostimulatory factor, interleukin X (IL-X), from a Protein Data Bank (PDB)-carrying lymphoblastoid cell line. IL-X proteins can be used to enhance the growth of cells in vitro, or to grow primary human B cell cultures to facilitate proliferation of these cell lines, as therapeutics or prophylactics, as molecular weight standards, as limit proteins in an assay, or in the detection of antibodies that are immunoreactive with IL-X. Recombinant sequences encoding the peptides could be used to produce recombinant peptides or they could be used as probes or primers for diagnostic and/or analytical laboratory chain reactions (PCR). Peptides such as DNA or RNA sizing standards. The present sequence represents the amino acid sequence of IL-X. | | |
| SQ | Sequence | 166 AA; | |
| | Query Match | 49.7%, Score: 868, E(-22), Length: 166, | |
| | Best Local Similarity | 100.0%; Prod No.: 90-597 | |
| | Matches: 166; Conservative | 0; Mismatches | 0; Indels |
| | Gaps | 0; Gaps | 0; |
| QY | 166 | MDGAPPVTHNCTAPCHLYVDFFSEFVDFSVLVEGLIADPEKRVIRIVLVS | 258 |
| Dd | 1 | LHQGPVPTLTNEGATKLGG; PHSASKYLSQPKLSAIFDPLKSLTGNALSS | 60 |
| QY | 166 | IPAEFYNSRVLISAGDAETELVLAKEGVYVGVSGEWMFGKPFLLVLRLEDA | 418 |
| Dd | 61 | PDAEPGFGLISGAFPPERISCKTYGPRGDPITTPKFRVLSLKHLPK | 120 |
| QY | 419 | VVELTRIDLEFFEQYHYVVVFCAEFWSHGDTCPFEWGVVAEN | 364 |
| Dd | 121 | YSLVLIHLKPGGYPVGRKKAKDPAASLQTPVPLAQACH | 166 |
| RESULT | 4 | | |
| AAP40854 | ID | AAP40856 standard; protein, 453 AA. | |
| AC | AAK40856; | | |
| XX | 07 MAR 1994 | (first entry) | |
| DE | 483 | expression associated with iqg | |

